

Metagenomic Analysis

An overview of the sequencing tools



TRAINING, DETERMINATION, DEDICATION...

and now---IT'S GO TIME !!!

The jargon

- Raw reads
- Unassembled vs assembled
- Read based
- K-mer
- Reference

The objective

- 16S rRNA amplicon
 - OTU table (counts per “species”)
 - Classification (“species” taxonomy)
 - Metadata (sample specific information)

The objective

- Metagenomic
 - Gene/genome count table (counts per “species”)
 - Classification (gene taxonomy/function)
 - Metadata (sample specific information)

Getting the most out of your data

ID, Abundance, Function

Complex Samples

16S rRNA amplicon sequencing

Pros:

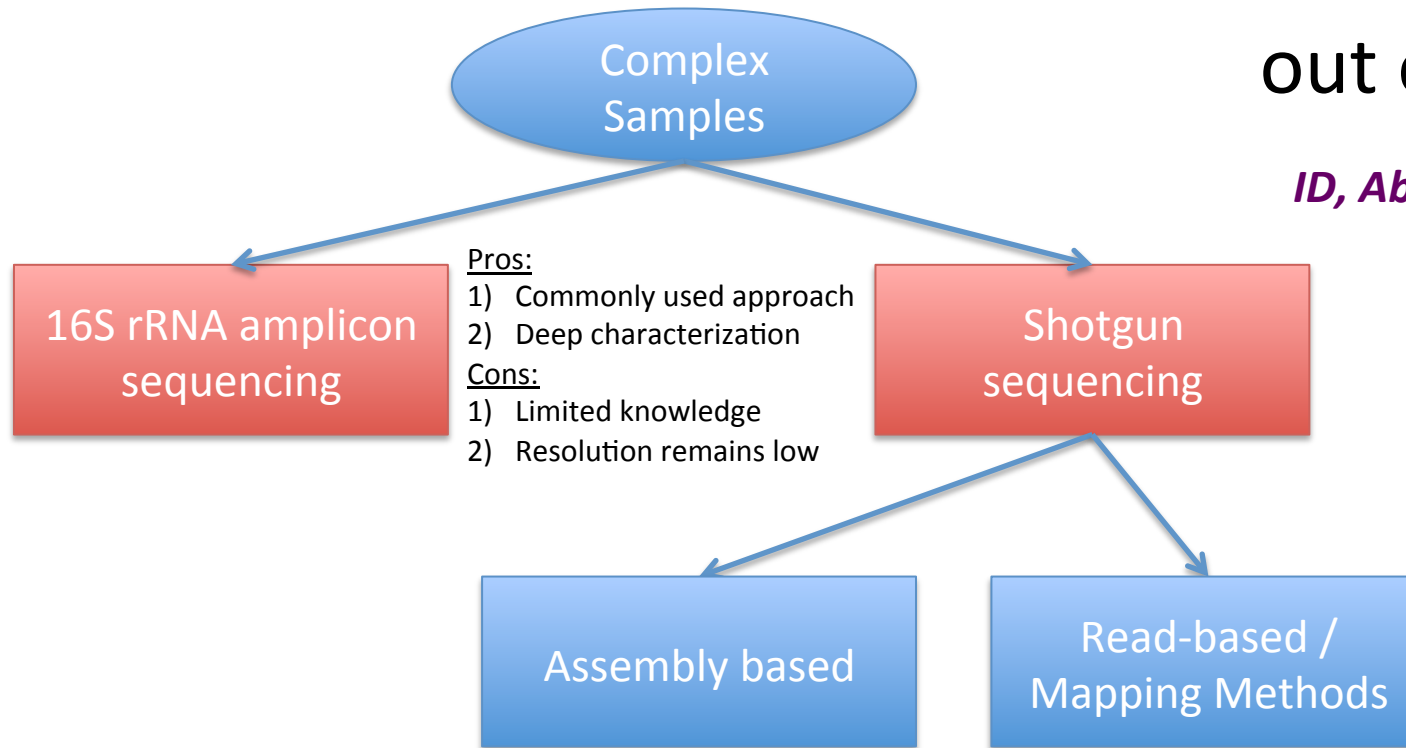
- 1) Commonly used approach
- 2) Deep characterization

Cons:

- 1) Limited knowledge
- 2) Resolution remains low

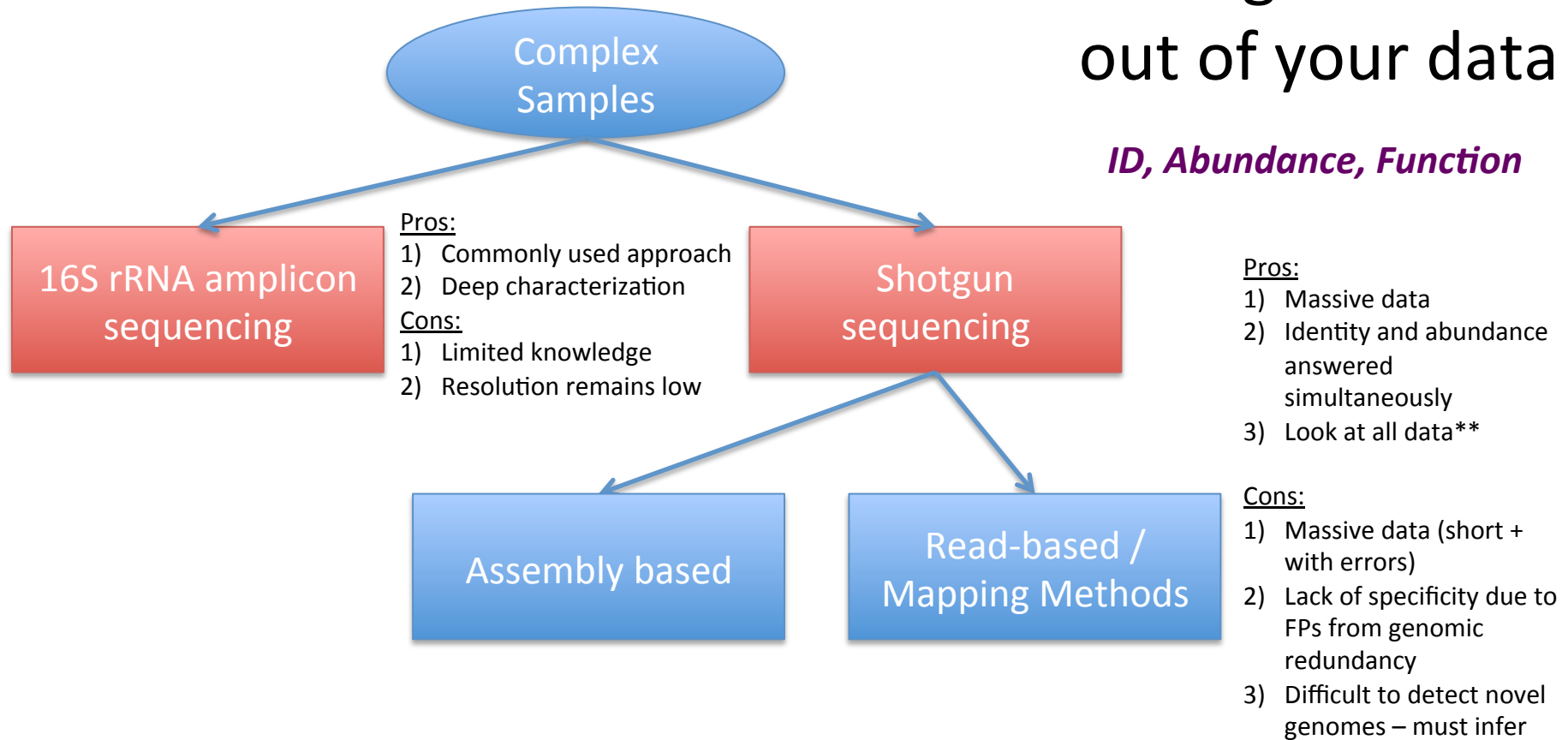
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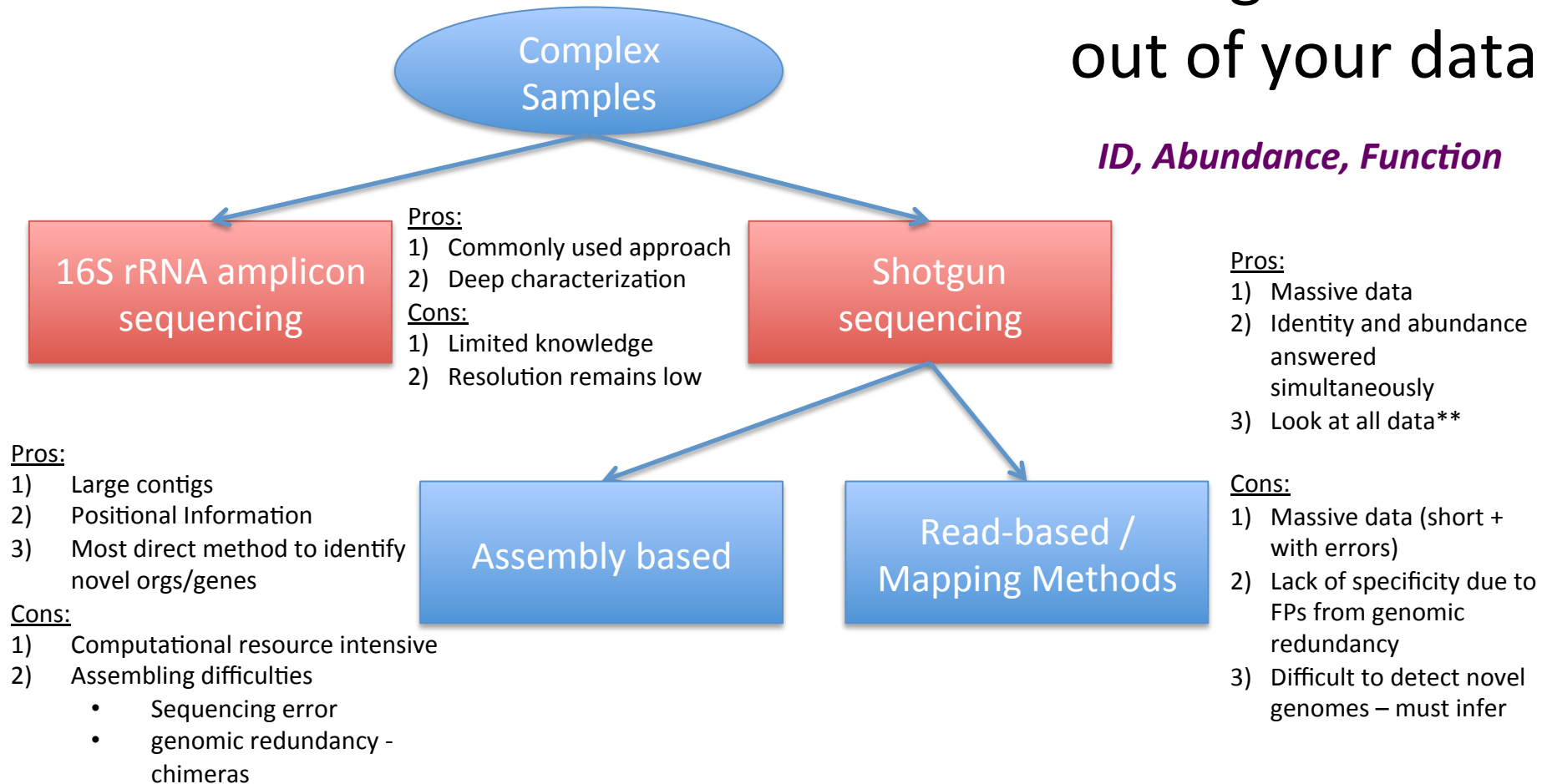
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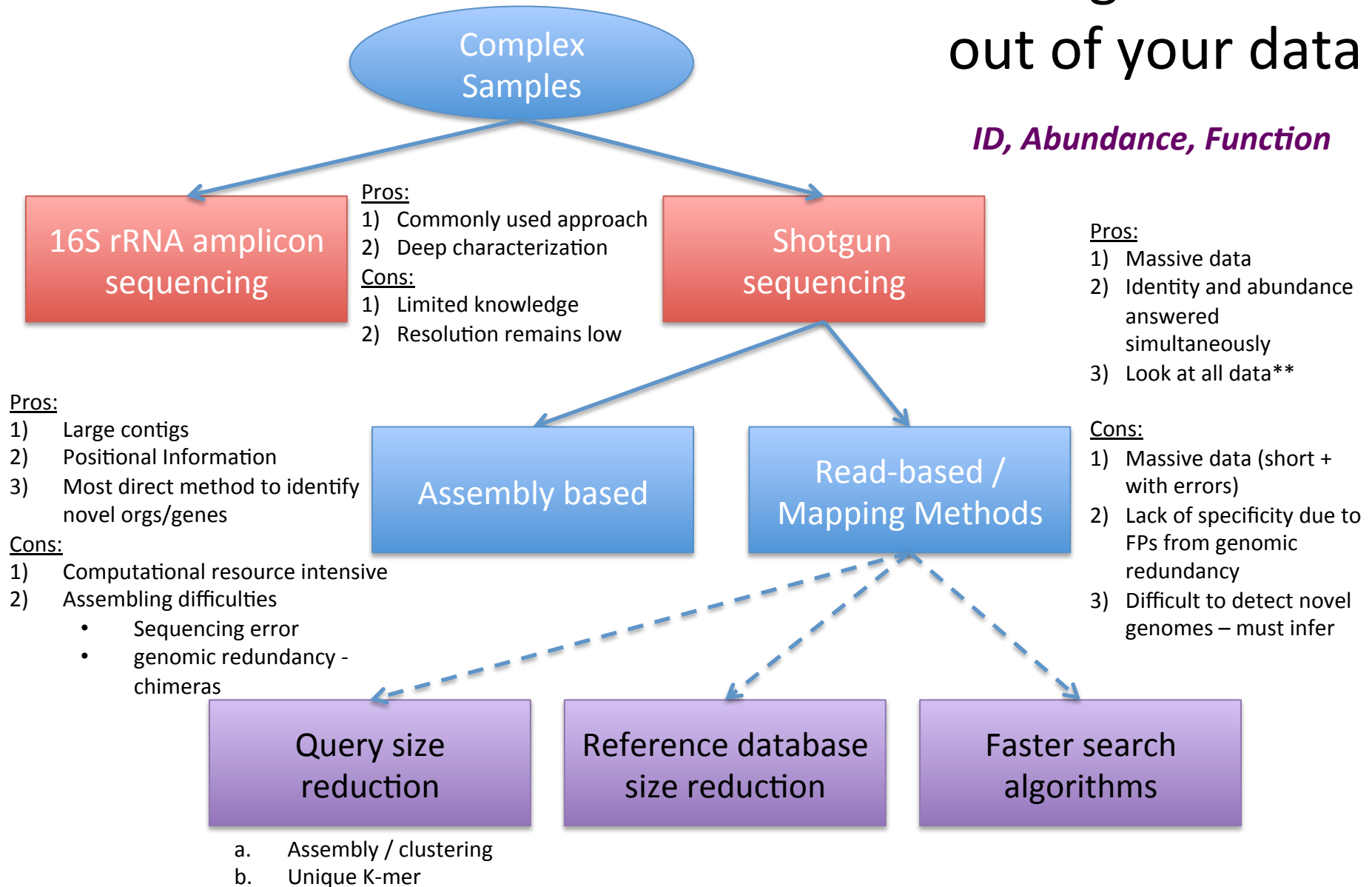
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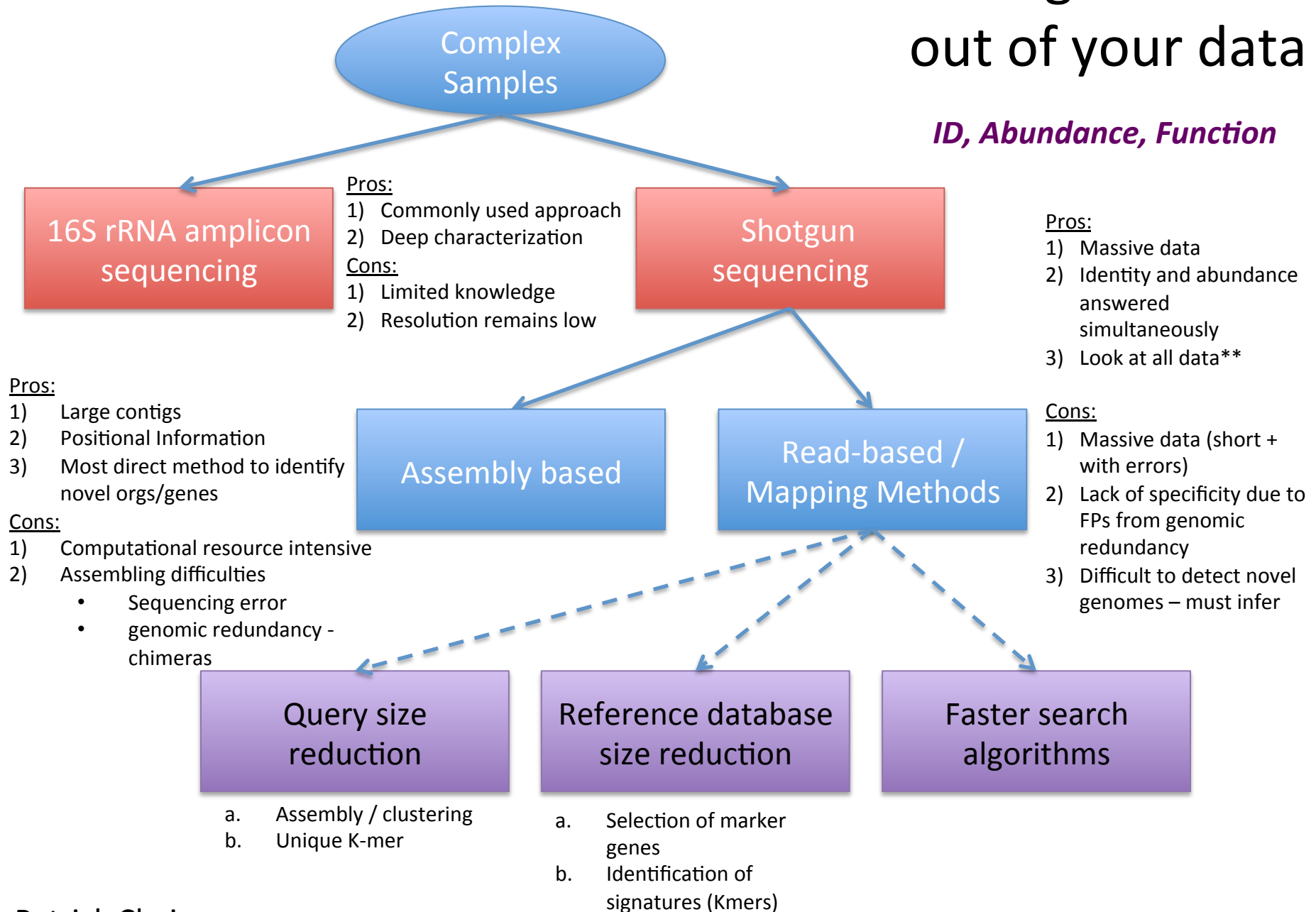
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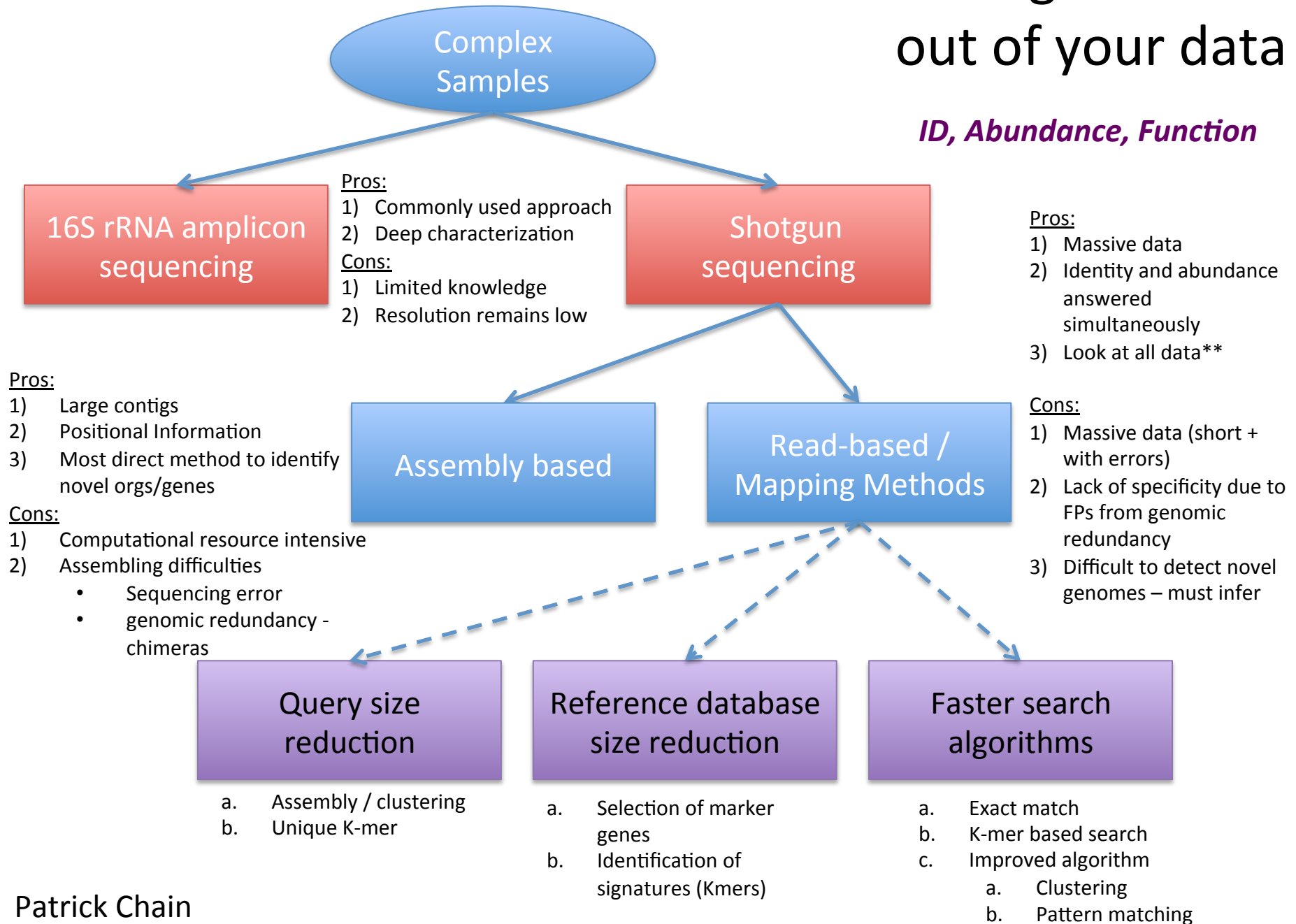
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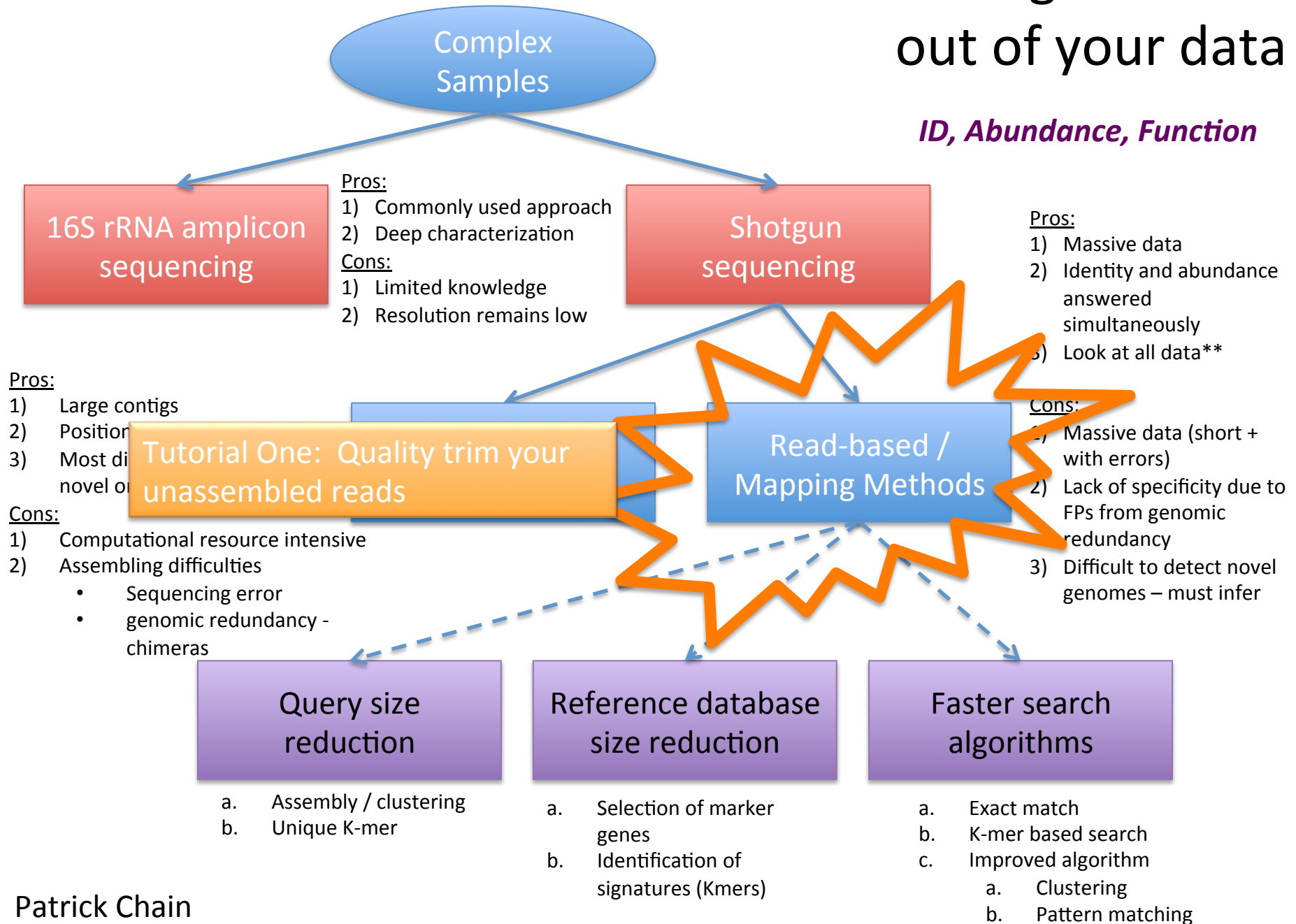
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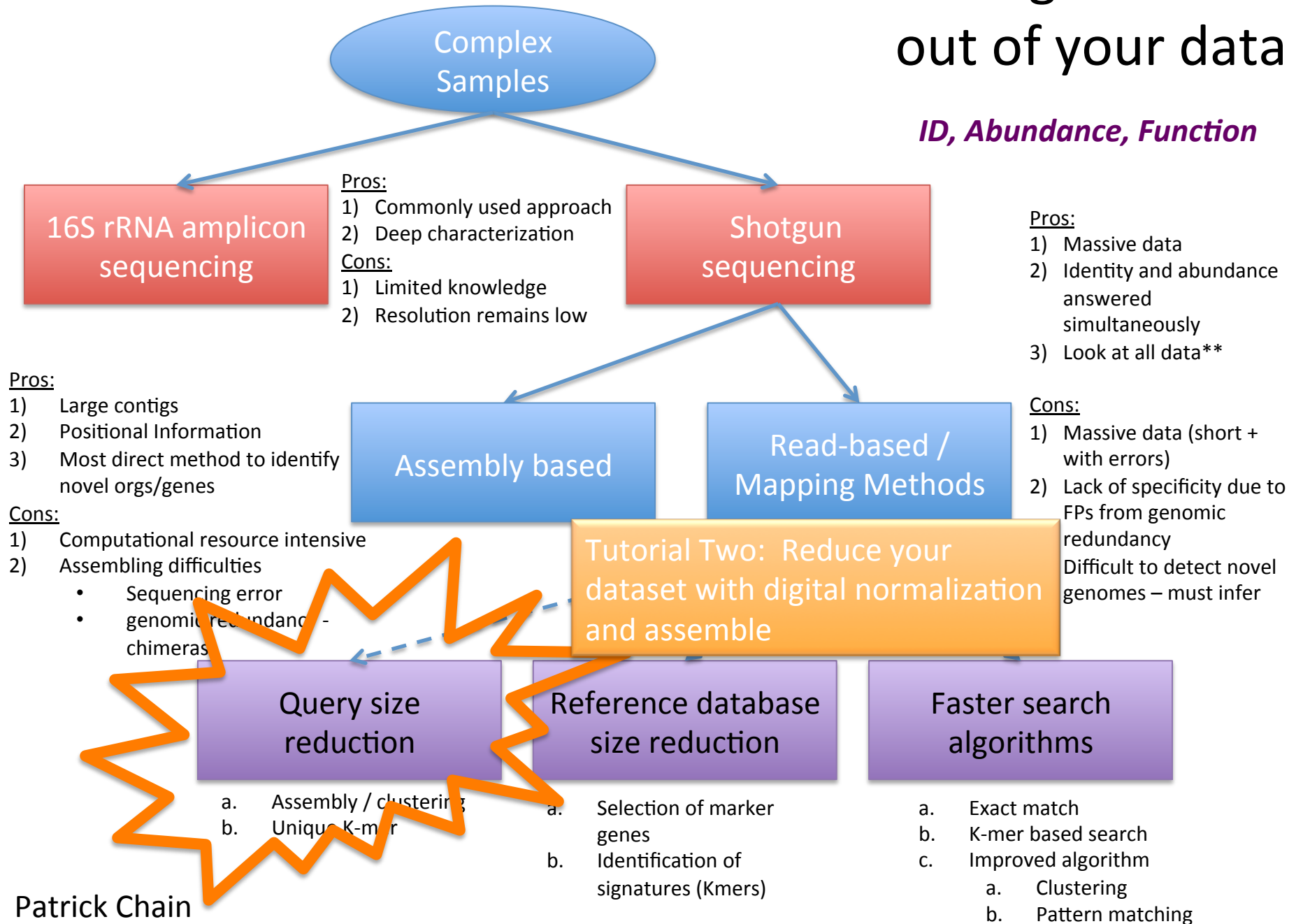
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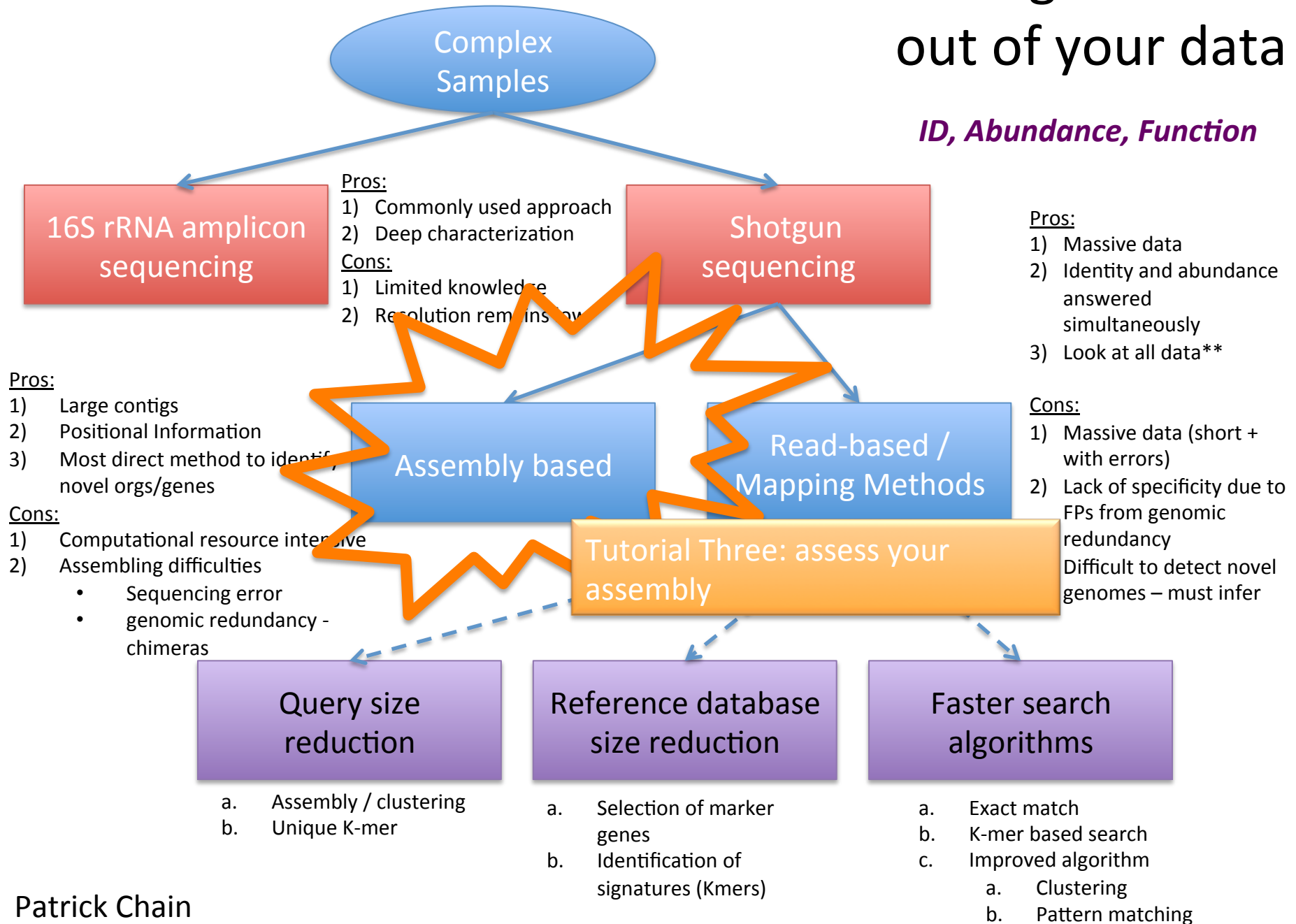
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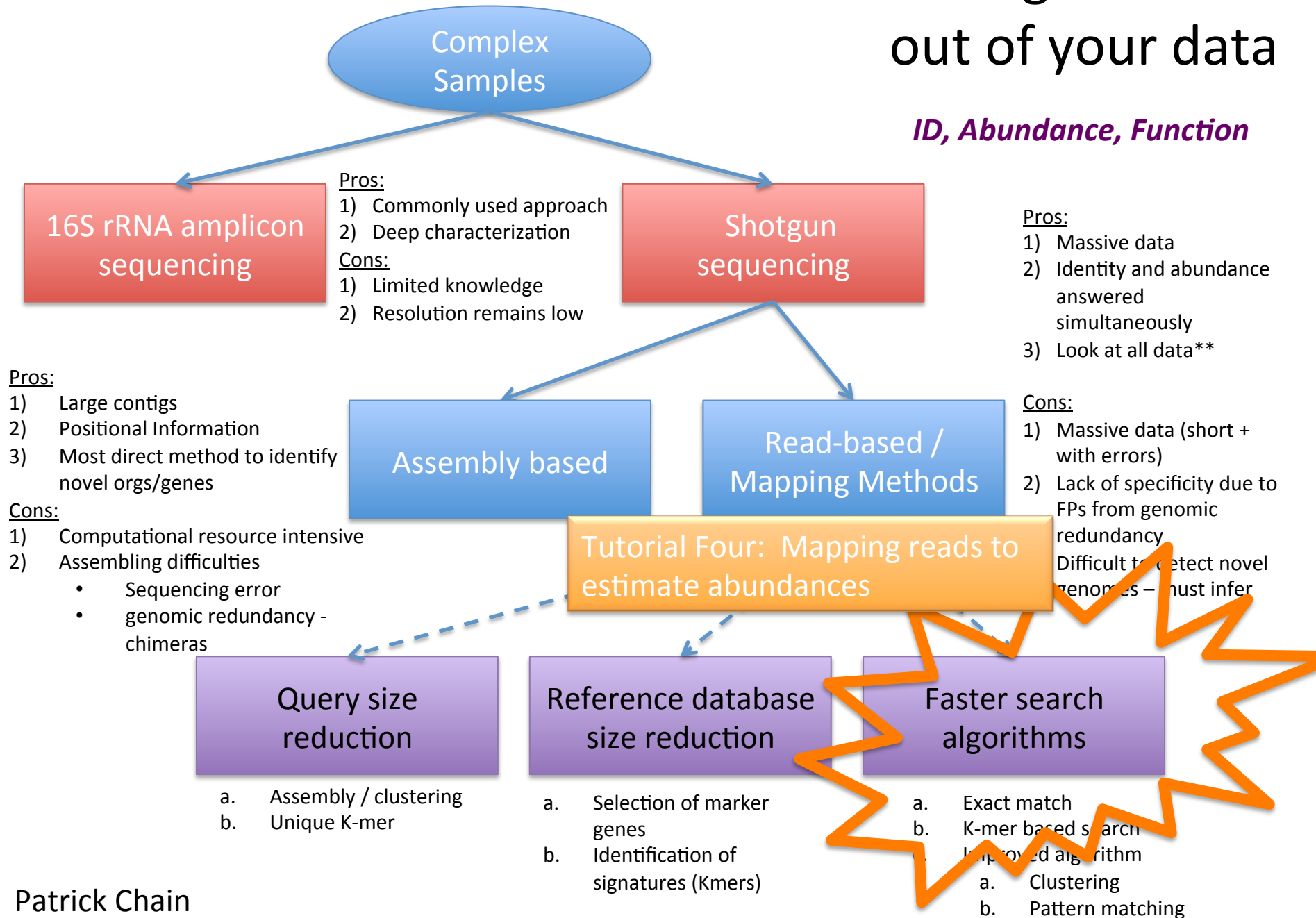
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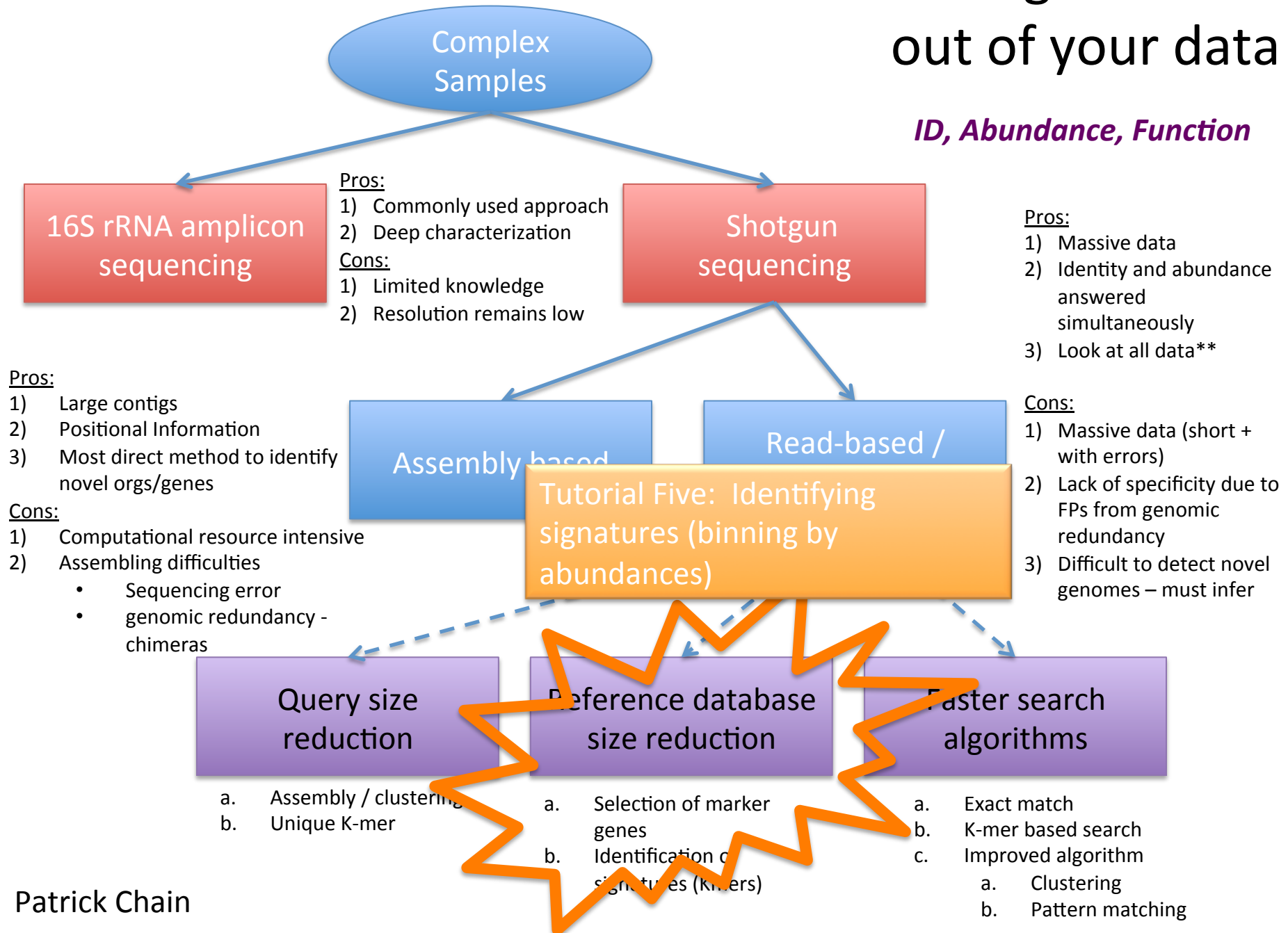
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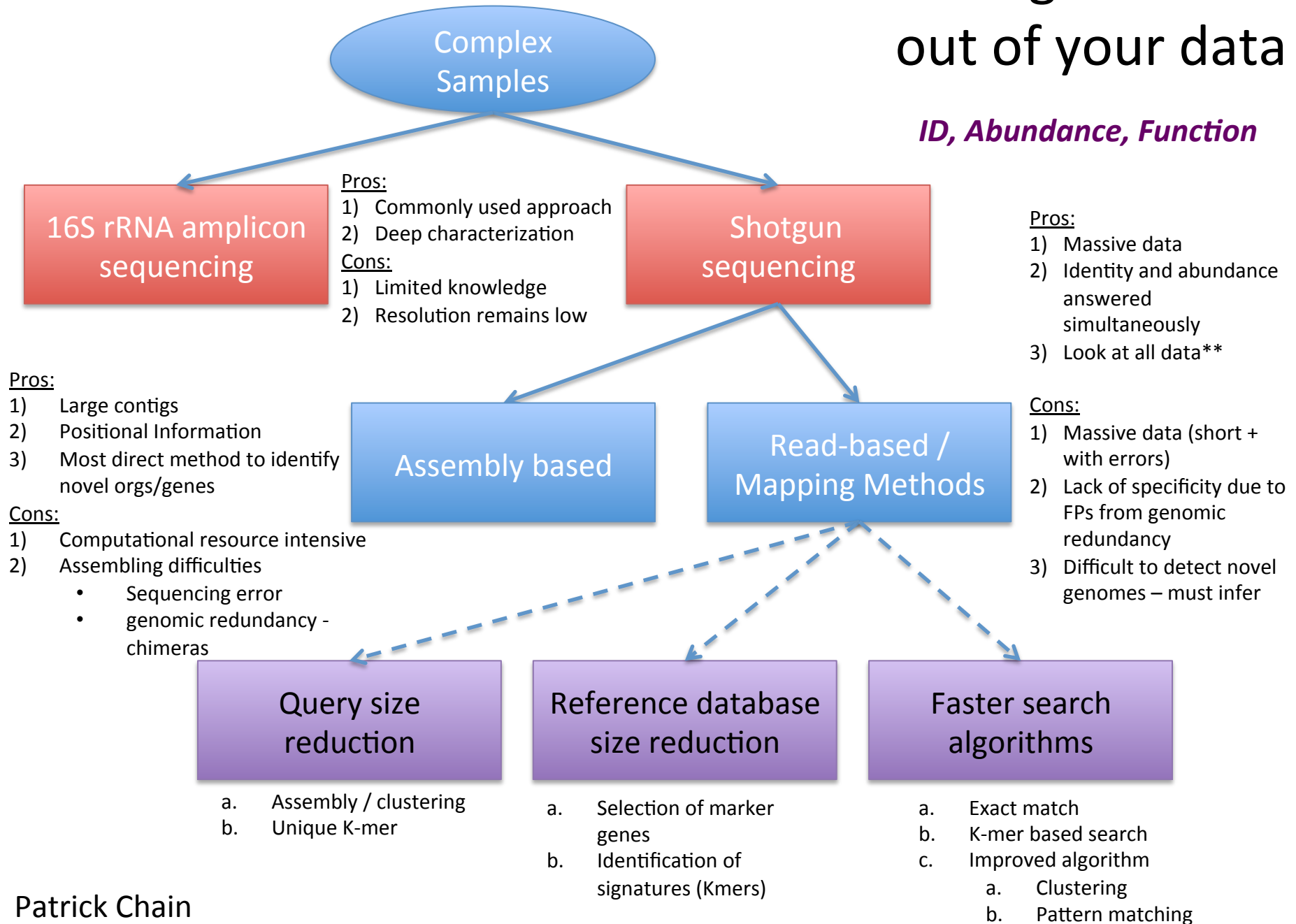
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So let's do some learning...

